

Eig. 1 A

131	P	V	Q	L	T	K	E	S	E	P	S	A	R	-	-	-	T	K	F	Y	F	E	Q	S	W
130	P	V	R	L	T	Q	L	P	E	N	G	G	W	N	A	P	I	T	D	F	Y	F	Q	C	D
156	P	V	S	L	T	T	P	K	E	P	-	-	C	T	V	T	K	F	Y	F	Q	E	D	Q	
155	P	V	G	L	T	N	T	P	K	A	A	-	-	V	K	V	T	K	F	Y	F	Q	Q	D	Q
137	P	V	S	L	T	N	M	P	D	E	G	-	-	V	M	V	T	K	F	Y	F	Q	E	D	E
137	P	V	S	L	T	N	M	P	D	E	G	-	-	V	M	V	T	K	F	Y	F	Q	E	D	E

Decoration 'id-consensus': Box residues that match the Consensus exactly.

Fig. 1B



FIGURE 2B

910	920	930	940	950	960
TAGCCTTGTG	CCCCAAACC	AAGCTCATCC	TGCTCAGGGT	CTATGGTAGG	CAGAATAATG
TCCCCGAAA	TATGTCCACA	TCCTAATCCC	AAGATCTGTG	CATATGTTAC	CATACATGTC
CAAAGAGGTT	TTGCAAATGT	GATTATGTTA	AGGATCTTGA	AATGAGGAGA	CAATCCTGGG
TTATCCTTGT	GGGCCTCAGTT	TAATCACAAAG	AAGGAGGCAG	GAAGGGAGAG	TCAGAGGAGAG
AATGGAAGAT	ACCATGCTTC	TAATTGTGAA	GATGGAGTGA	GGGGCCTTGA	GCCAACATAT
					1200
1210	1220	1230	1240	1250	1260
GCTGTGTT	TTAGAAAGGAG	GAAAGCCAA	GGGAACGGAT	TCTCCTCTAT	AGTCCTCCGGA
AGGAACACAG	CTCTTGACAC	ATGGGATTCA	GCTCAGTGAC	ACCCATTCA	GACTCTGAC
CTCCACAACT	ATAAAATAAT	AAACTGTGT	TATTGTAAAC	CTCTGG	1366

FIGURE 3

SEQ ID NO. : 13

10 MNGLGNPCSP WLSGSKPQHV CLWLHPASFS NCPSSLPISE DQTPLIAGMC  
SLPMARYII KYADQKALYT RDGQLLVGDP VADNCCAEKI CTLPNRGLDR 50  
TKVPIFLGIQ GGSRCLACVE TEEGPSLQLE DVNIEELYKG GEAATRFTFF 100  
QSSGSAFRL EAAAWPGWFL CQPAEPQQPV QLTKESEPSA RTKFYFEQSW 150  
200

FIGURE 4A

SEQ ID NO. : 14

10	GGCAGTGGGA	CTGGGTTGA	GCTGGGCTTA	TCTCCAACT	GTGAGGGAGG	CTACAGCACA	60
	CTCCACCCA	CTCTCAGGGC	TGGGAATTGT	TGTGGCTCAG	CTATTGAAA	GAATCTGTTT	120
	TCCAGTTCT	CAGAACCCAGC	GCAAGCACAC	ACATCCCAGG	CTCACACCCC	TGTTGGCTGG	180
	ACTTGCTCC	GGATAGCCTC	AGTCAGGGAG	AGGCAGAGCT	GCCTGGAGCC	TGCTGGGCTG	240
	GTGGAAGCCT	TGGTGGATTC	TGGCAGGCCA	ATTATAGACG	AATGGCCTGG	GGAACCCGTG	300
310	CAGCCCCGTGG	CTGAGTGGTT	CTAACCCCCA	GCACCGTCTGC	CTCTGGCTTC	ACCCAGCCCTC	360
	CTTTTCTAAC	TGCCCTTCTC	TCCTCCCCAT	CAGTGAGGAC	CAGACACCAC	TGATTGCAGG	420
	AATGTGTTC	CTCCCCATGG	CAAGATACTA	CATAATTAAA	TATGCAGACC	AGAAGGCTCT	480
	ATACACAAGA	GACGGCCAGC	TGCTGGTGG	AGATCCTGTT	GCAGACAACT	GCTGTGCAGA	540
	GAAGATCTGC	ACACTTCCCA	ACAGAGGCTT	GGACCCGACC	AAGGTCCCCA	TTTCCTGGG	600
610	GATCCAGGGA	GGGAGCCGCT	GCCTGGCATG	TGTGGAGACA	GAAGAGGGGC	CTTCCCTACA	660
	GCTGGAGGAT	GTGAACATG	AGGAACCTGTA	CAAAGGTGGT	GAAGAGGCCA	CACGCTTCAC	720
	CTTCTTCCAG	AGCAGCTCAG	GCTCCGGCTT	CAGGCTTGAG	GCTGCTGGCCT	GGCCTGGCTG	780
	GTTCCCTGT	GGCCCGGGCAG	GCCAGTACAG	CTCACCAAGG	AGAGTGAGCC	840	
	CTCAGCCGT	ACCAAGTTT	ACTTGAACA	GAGCTGGTAG	GGAGACAGGA	AACTGGCGTTT	900

FIGURE 4B

910	920	930	940	950	960
TAGGCCCTGTG	CCCCAAACC	AAGCTCATCC	TGCTCAGGGT	CTATGGTAGG	CAGAATAATG
TCCCCGAAA	TATGTCACCA	TCCTAATCCC	AAGATCTGTG	CATATGTTAC	CATACATGTC
CAAAGAGGTT	TTGCAAATGT	GATTATGTTA	AGGATCCTGA	AATGAGGAGA	CAATCCTGGG
TTATCCTTGT	GGGCTCAGTT	TAATCACAAAG	AAGGAGGCAG	GAAGGGAGAG	TCAGAGGAGAG
AATGGAAGAT	ACCATGCTTC	TAATTGCTGAA	GATGGAGTGA	GGGGCCCTTGA	GCCAAACATAT
1210	1220	1230	1240	1250	1260
GCTGTGTT	TTAGAAGGAG	GAAAAGCCAA	GGGAACGGAT	TCTCCTCTAT	AGTCCTCCGGA
AGGAACACAG	CTCTTGACAC	ATGGGATTCA	GCTCAGTGTGAC	ACCCATTCA	GACTTCTGAC
CTCCACAACT	ATAAAATAAT	AAACTTGTGT	TATTGTAAAC	CTCTGG	1366

Figure 5

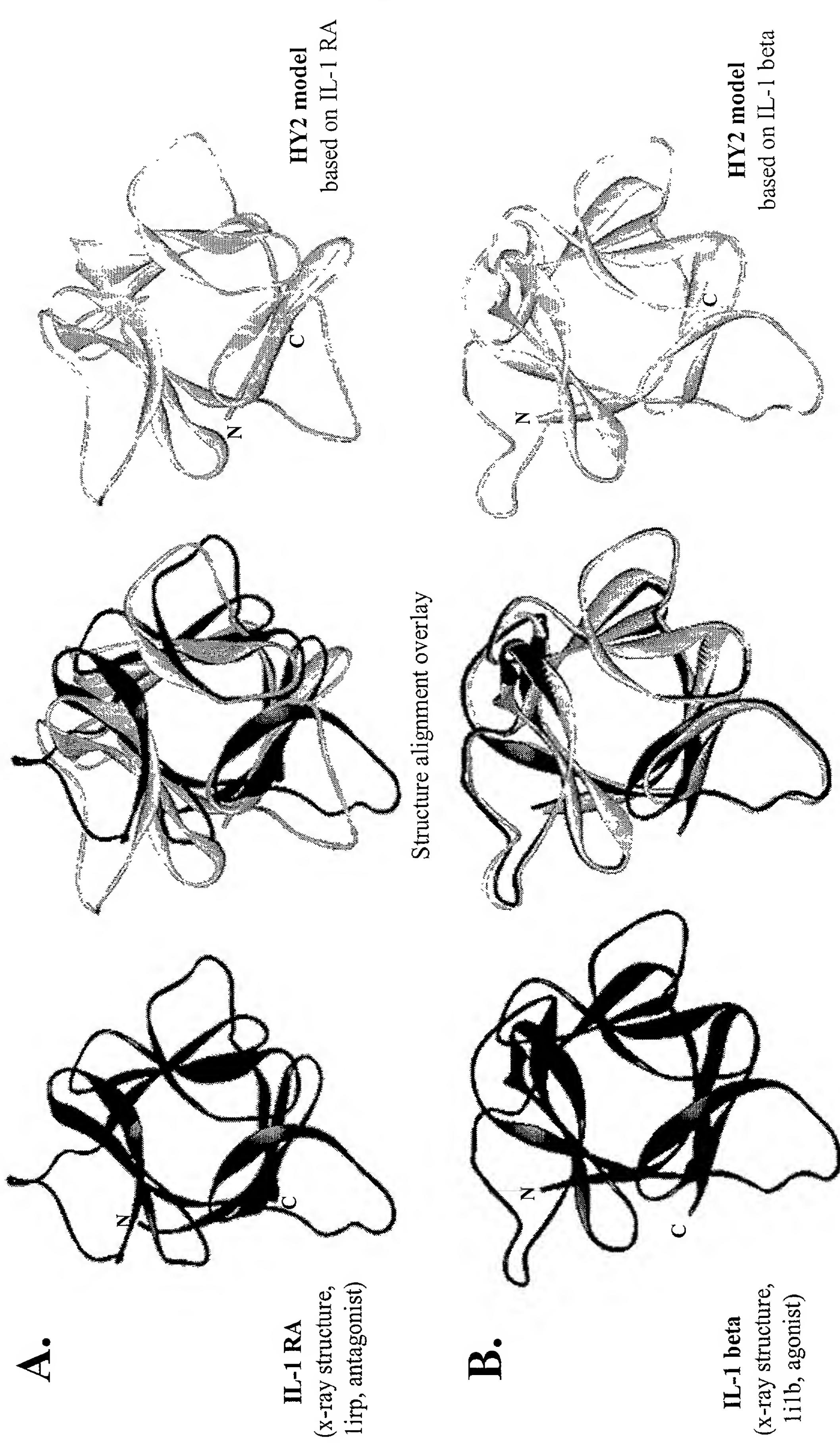


Figure 6

## Sequence Alignment based on 2<sup>o</sup> Structure

### HY2 and IL-1 RA (antagonist)

IL-1RA:	10	MQAFRIWDVNQKTFYLRNNNQLVAGYLQGPNNLEEKIDVVPIEPHA - - - - -	- - 4 - - >	- - 5 - >
		+ + I +QK Y R+ QL+ G	N EKI + + P	+FLGI GG
Hy2	: 1	ARYI <sup>1</sup> IKYADQKALYTRDGQ <sup>2</sup> LLVGDPVADNCC-AEKICILPNRGLDRTKVP <sup>3</sup> IFLGIQGG <sup>4</sup> S 59		SEQ ID NO: 22
IL-1RA:	65	- - - 6 - - > - - - 7 - - - > variable dom.	- - 8 - - > - - 9 - >	- 10 - >
		MCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 124		SEQ ID NO: 21
		CL+CV++ + LQLE VNI +L + RF F + S SG	E+AA PGWFLC	
Hy2	: 60	RCLACVETEEGPSLQLLEDVNIEELYKGGEATRFFFQSSSSGSAFRLEAAAWPGWFLCGP 119		SEQ ID NO: 22
IL-1RA:	125	- - 11 - > - - 12 - - >		
		MEADQPVSLTNMPDEGVMVTKFYFQEDE 152		SEQ ID NO: 21
		E QPV LT E TKFYF++		
Hy2	: 120	AEPQQPVQLT <sup>1</sup> KES - EPSART <sup>2</sup> KFYFEQSW 146		SEQ ID NO: 22

- β-strand - - >

**SEQ ID NO:22 = amino acid 7-153  
of SEQ ID NO: 2**

Figure 7

## Sequence Alignment based on 2<sup>o</sup> Structure

### Hy2 and IL-1 beta (agonist)

IL-1 $\beta$ :	3	VRSLNCTLRDSQQKS <u>L</u> VMMSGP <u>Y</u> EILKALH <u>L</u> QGQDMEQQVFSMS <u>F</u> VQGEE <u>S</u> ND <u>K</u> I <u>P</u> V <u>A</u> L <u>G</u> L	SEQ ID NO: 23
		+ + + + QK+L +L + + + + G + + + + G + + + + K+P+ LG+	
Hy2 :	1	PMARYYI <u>I</u> KYAD <u>Q</u> KALYTRDG-Q <u>LL</u> VG <u>D</u> P <u>V</u> ADNCCAEK-I <u>C</u> IL <u>P</u> NR <u>G</u> L <u>D</u> R <u>T</u> -K <u>V</u> P <u>I</u> F <u>L</u> G <u>I</u>	SEQ ID NO. 24
		- - - - 6 - - - > - - - - 7 - - - > - - - - 8 - - - > - - - - 10 - - - > - - - - 11 -	
IL-1 $\beta$ :	63	KEKNLYLSCVLKDDKPTLQLESVDP <u>K</u> N-YPKKKMEKRFV <u>F</u> N <u>K</u> I <u>E</u> INNN <u>K</u> LE <u>F</u> ESA <u>Q</u> F <u>P</u> N <u>W</u> Y	SEQ ID NO: 23
		+ + L+CV ++ P+LQLE V+ + Y + RF F + + E+A + P W+	
Hy2 :	58	QGGSR <u>C</u> LA <u>V</u> E <u>T</u> E <u>E</u> G <u>P</u> SLQ <u>E</u> D <u>V</u> N <u>I</u> E <u>E</u> LY <u>K</u> G <u>G</u> EE <u>E</u> AT <u>R</u> F <u>T</u> F <u>F</u> Q <u>S</u> SS <u>S</u> SG <u>S</u> A <u>F</u> R <u>L</u> E <u>A</u> A <u>W</u> P <u>G</u> WF	SEQ ID NO: 24
		- - > - - 12 - - > - - - - 13 - - - >	
IL-1 $\beta$ :	122	1ST <u>S</u> QA <u>E</u> N <u>M</u> P <u>V</u> FL <u>G</u> GT <u>K</u> GG <u>Q</u> D <u>I</u> T <u>D</u> F <u>T</u> M <u>Q</u> F <u>V</u> SS	SEQ ID NO: 23
		+ PV L T F +	
Hy2 :	118	LCGPAEPQQPPVQLTKESEP <u>SART</u> <u>K</u> F <u>Y</u> F <u>E</u> Q <u>SW</u>	SEQ ID NO: 24

-  $\beta$  - strand - - >

SEQ ID NO: 24 = amino acid 5-153  
of SEQ ID NO: 2